

## Curriculum Vitae

Mark W. Perlin, PhD, MD, PhD  
*DNA evidence interpretation and the likelihood ratio*

Cybergenetics, Corp.  
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### Positions Held

Cybergenetics, Corp.	chief scientific officer & chief executive officer	1996-present	Comput. Bioscience
Carnegie Mellon University	senior research scientist	1995-1996	Computer Science
Carnegie Mellon University	research computer scientist	1992-1995	Computer Science
Carnegie Mellon University	research associate	1988-1992	Computer Science
Carnegie Mellon University	visiting researcher	1986-1988	Computer Science
Pittsburgh NMR Institute	research scientist	1985-1986	Comput. Radiology
Mercy Hospital, Pittsburgh, PA	transitional resident	1984-1985	Medicine/Radiology
IBM/Watson Research Yorktown, NY	post-doctoral fellow	1984-1984	Mathematics

### Education and Training

Carnegie Mellon University, Pittsburgh, PA	Ph.D.	1991	Computer Science
The University of Chicago Pritzker School of Medicine	M.D.	1984	Medicine
City University of New York Graduate School	Ph.D.	1982	Mathematics
Harpur College/SUNY, Binghamton, NY	B.A.	1977	Chemistry

### Professional Societies

American Academy of Forensic Sciences  
 American Society of Human Genetics  
 American Statistical Association

### Honors and Awards

Keynote Speaker, International Conference on Forensic Inference and Statistics, 2014  
 Keynote Speaker, International Conference on Forensic Research and Technology, 2012  
 Keynote Speaker, Duquesne University Summer Research Symposium, 2010  
 Keynote Speaker, ACM Symposium on Software Reusability, 2001  
 Keynote Speaker, SRI Biotechnology Conference, 1997  
 CUNY Alumnus Achievement Award, 1990  
 Phi Beta Kappa, 1977  
 Eagle Scout, 1974  
 Bausch and Lomb Science Award, 1973

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## Patents

M. W. Perlin, "Method and system for DNA mixture analysis," U.S. Patent #8,898,021, Nov. 2014  
 M. W. Perlin, "Method and system for DNA mixture analysis," E.P.O. Patent #1,229,135, Jan. 2014  
 M. W. Perlin, "Method for DNA mixture analysis," U.S. Patent #6,807,490, Oct. 2004  
 M. W. Perlin, "Method and system for genotyping," U.S. Patent #6,750,011, Jun. 2004  
 M. W. Perlin, "Method and system for sequencing genomes," U.S. Patent #6,068,977, May 30, 2000.  
 M. W. Perlin, "Method and system for genotyping," U.S. Patent #6,054,268, Apr. 15, 2000.  
 M. W. Perlin, "Method and system for genotyping," U.S. Patent #5,876,933, Mar. 2, 1999.  
 M. W. Perlin, "A system and method for producing maps and cloning genes therefrom," U.S. Patent #5,622,823, Apr. 22, 1997.  
 M. W. Perlin, "Method and system for sequencing genomes," U.S. Patent #5,604,100, Feb. 18, 1997.  
 M. W. Perlin, "Method and system for genotyping," U.S. Patent #5,580,728, Dec. 3, 1996.  
 M. W. Perlin, "Method and system for genotyping," U.S. Patent #5,541,067, Jul. 30, 1996.

## Publications

### *Journal (30)*

M. W. Perlin, J. Hornyak, G. Sugimoto, and K. Miller. "TrueAllele<sup>®</sup> genotype identification on DNA mixtures containing up to five unknown contributors." *Journal of Forensic Sciences*. 2015;*in press*.

M. W. Perlin, K. Dormer, J. Hornyak, L. Schiermeier-Wood, and S. Greenspoon, "TrueAllele<sup>®</sup> Casework on Virginia DNA mixture evidence: computer and manual interpretation in 72 reported criminal cases." *PLOS ONE*, 9(3):e92837, 2014.

M. W. Perlin, J. L. Belrose, and B. W. Duceman, "New York State TrueAllele<sup>®</sup> Casework validation study." *Journal of Forensic Sciences*, 58(6):1458-1466, 2013.

J. Ballantyne, E. K. Hanson and M. W. Perlin. "DNA mixture genotyping by probabilistic computer interpretation of binomially-sampled laser captured cell populations: combining quantitative data for greater identification information." *Science & Justice*, 53(2):103-114, 2013.

M. W. Perlin, "When good DNA goes bad," *Journal of Forensic Research*, S11:003, DOI 10.4172/2157-7145.S11-003, 2013.

M. W. Perlin, M. M. Legler, C. E. Spencer, J. L. Smith, W. P. Allan, J. L. Belrose and B. W. Duceman. "Validating TrueAllele<sup>®</sup> DNA mixture interpretation." *Journal of Forensic Sciences*, 56(6) 1430-1447, 2011.

M. W. Perlin and A. Sinelnikov, "An information gap in DNA evidence interpretation." *PLoS ONE*, 4(12):e8327, 2009.

M. W. Perlin, J. B. Kadane and R. W. Cotton, "Match likelihood ratio for uncertain genotypes." *Law, Probability and Risk*, 8(3):289-302, 2009.

S. Y. Hill, S. Shen, N. Zezza, E. K. Hoffman, M. W. Perlin and W. Allan. "A genome wide search for alcoholism susceptibility genes." *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics* 128B(1): 102-113, 2004.

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M. W. Perlin and B. Szabady, "Determining sequence length or content in zero, one, and two dimensions," *Human Mutation*, 19(4), 2002.

M. W. Perlin and B. Szabady, "Linear mixture analysis: a mathematical approach to resolving mixed DNA samples," *Journal of Forensic Sciences*, 46(6), pp. 1372-77, 2001.

B. Pálsson, F. Pálsson, M. Perlin, H. Gubjartsson, K. Stefánsson, and J. Gulcher, "Using quality measures to facilitate allele calling in high-throughput genotyping," *Genome Research*, 9(10): 1002-1012, 1999.

G. Lancia and M. Perlin, "Genotyping of pooled microsatellite markers by combinatorial optimization techniques," *Discrete Applied Math.*, vol. 88, no. 1-3, pp. 291-314, 1998.

M. W. Perlin, "Reliable genome maps from unreliable data: BIN-SORT mapping of cloned DNA fragments," *Math. Model. Sci. Comp.*, 1998.

M. W. Perlin, "Rapid construction of genome maps," *Nature Med.*, vol. 3, no. 9, pp. 1046-1048, 1997.

C. Andrews, B. Devlin, M. Perlin, and K. Roeder, "Binning clones by hybridization with complex probes: statistical refinement of an inner product mapping method," *Genomics*, vol. 41, no. 2, pp. 141-154, 1997.

M. W. Perlin, G. Lancia, and S.-K. Ng, "Toward fully automated genotyping: genotyping microsatellite markers by deconvolution," *Am. J. Hum. Genet.*, vol. 57, no. 5, pp. 1199-1210, 1995.

M. W. Perlin, D. J. Duggan, K. Davis, J. E. Farr, R. B. Findler, M. J. Higgins, N. J. Nowak, G. A. Evans, S. Qin, J. Zhang, T. B. Shows, M. R. James, and C. W. Richard III, "Rapid construction of integrated maps using inner product mapping: YAC coverage of human chromosome 11," *Genomics*, vol. 28, no. 2, pp. 315-327, 1995.

H. Kobayashi, T. C. Matise, M. W. Perlin, H. G. Marks, and E. P. Hoffman, "Towards fully automated genotyping: use of an X linked recessive spastic paraplegia family to test alternative analysis methods," *Hum. Genet.*, vol. 95, pp. 483-490, 1995.

M. W. Perlin, M. B. Burks, R. C. Hoop, and E. P. Hoffman, "Towards fully automated genotyping: allele assignment, pedigree construction, phase determination, and recombination detection in Duchenne muscular dystrophy," *Am. J. Hum. Genet.*, vol. 55, no. 4, pp. 777-787, 1994.

M. W. Perlin, "Visualizing dynamic artificial intelligence algorithms and applications," *Artificial Intelligence Tools*, vol. 3, no. 2, pp. 289-307, 1994.

T. C. Matise, M. W. Perlin, and A. Chakravarti, "Automated construction of genetic linkage maps using an expert system (MultiMap): application to 1268 human microsatellite markers," *Nature Genetics*, vol. 6, no. 4, pp. 384-390, 1994.

M. W. Perlin and A. Chakravarti, "Efficient construction of high-resolution physical maps from yeast artificial chromosomes using radiation hybrids: inner product mapping," *Genomics*, vol. 18, no. 2, pp. 283-289, 1993.

M. W. Perlin, "Factored arc consistency for RETE match," *Artificial Intelligence Tools*, 1993.

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E. Kanal and M. Perlin, "Computer-based magnetic resonance imaging tutorial," *Amer. J. Neuroradiology*, vol. 13, pp. 1527-1534, 1992.

M. W. Perlin, "Arc consistency for factorable relations," *Artificial Intelligence*, vol. 53, no. 2-3, pp. 329-342, 1992.

M. W. Perlin, "Transforming recursive processes into efficient algorithms: call-graph caching for artificial intelligence," *Artificial Intelligence Tools*, vol. 1, 1992.

M. W. Perlin, "Transforming conjunctive match into RETE: a call-graph caching approach," *Int. Journal of Software Engineering and Knowledge Engineering*, vol. 1, no. 4, 1991.

M. W. Perlin, "Topologically traversing the RETE network," *Applied Artificial Intelligence*, vol. 4, pp. 155-177, 1990.

E. F. Feig, F. Greenleaf, and M. W. Perlin, "Magnetic resonance imaging with non-uniform fields," *Physics in Medicine and Biology*, vol. 10, pp. 1091-1099, 1986.

*Conference (18)*

M. W. Perlin, "DNA mapping the crime scene: do computers dream of electric peaks?," in the *Proceedings of Promega's Twenty Third International Symposium on Human Identification*, Nashville, TN, 2012.

M. W. Perlin, "Combining DNA evidence for greater match information." *Forensic Science International: Genetics Supplement Series*, 3(1):e510–e511, 2011.

M. W. Perlin, "Investigative DNA databases that preserve identification information." *Forensic Science International: Genetics Supplement Series*, 3(1):e484–e485, 2011.

M. W. Perlin, "Explaining the likelihood ratio in DNA mixture interpretation," in the *Proceedings of Promega's Twenty First International Symposium on Human Identification*. San Antonio, TX, 2010.

M. W. Perlin, "Scientific validation of mixture interpretation methods," in the *Proceedings of Promega's Seventeenth International Symposium on Human Identification*. Nashville, TN, 2006.

M. W. Perlin, "Real-time DNA investigation," in the *Proceedings of Promega's Sixteenth International Symposium on Human Identification*. Dallas, TX, 2005.

M. W. Perlin, "Simple reporting of complex DNA evidence: automated computer interpretation," in the *Proceedings of Promega's Fourteenth International Symposium on Human Identification*. Phoenix, AZ, 2003.

M. W. Perlin, D. Coffman, C.A. Crouse, F. Konotop, and J.D. Ban, "Automated STR data analysis: validation studies," in the *Proceedings of Promega's Twelfth International Symposium on Human Identification*. Biloxi, MS, 2001.

M. W. Perlin, "An expert system for scoring DNA database profiles," in the *Proceedings of Promega's Eleventh International Symposium on Human Identification*. Biloxi, MS, 2000.

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M. W. Perlin, "Computer automation of STR scoring for forensic databases". *In* First International Conference on Forensic Human Identification in The Millennium, London, UK, The Forensic Science Service, 1999.

M. W. Perlin, and D. R. Richards, "Quantitative analysis of gel electrophoresis data for automated genotyping applications (Abstract)," *Amer. J. Hum. Genet.*, **57**(4 Supplement): A26, 1995.

D. K. Pathak, E. P. Hoffman, and M. W. Perlin, "Intelligent molecular diagnostics using PCR-based linked genetic markers," in *Second International Conference on Intelligent Systems for Molecular Biology*, Stanford, CA, pp. 331-339, 1994.

D. K. Pathak and M. W. Perlin, "Automatic computation of genetic risk," in *Proceedings of the Tenth Conference on Artificial Intelligence for Applications*, San Antonio, Texas, pp. 164-170, 1994.

M. W. Perlin, "Principled animation of artificial intelligence algorithms," in *Fifth Int. Conf. on Tools for Artificial Intelligence*, Boston, MA, IEEE Computer Society, 1993.

M. W. Perlin, "Incremental binding-space match: The linearized MatchBox algorithm," in *Third Int. Conf. on Tools for Artificial Intelligence*, San Jose, CA, IEEE Computer Society, November, 1991.

M. W. Perlin, "LR recursive transition networks for Earley and Tomita parsing," in *Proceedings of the 29th Association for Computational Linguistics Meeting*, Berkeley, CA, June, 1991."

M. W. Perlin, E. Kanal, and A. John, "A user interface for visualizing concepts in Magnetic Resonance Imaging," in *First Conference on Visualization in Biomedical Computing*, Atlanta, GA, May, 1990.

M. W. Perlin, "Call-Graph Caching: transforming programs into networks," in *Proc. of the Eleventh Int. Joint Conf. on Artificial Intelligence*, Detroit, Michigan, Morgan Kaufmann, August, 1989, pp. 122-128.

#### *Magazine (4)*

M. W. Perlin and K. W. P. Miller, "Kern County resolves the DNA mixture crisis." *Forensic Magazine*, 11(4):8-12, 2014.

M. W. Perlin, "Easy reporting of hard DNA: computer comfort in the courtroom." *Forensic Magazine*, 9(4):32-37, 2012.

M. W. Perlin and J. Galloway, "Computer DNA evidence interpretation in the Real IRA Massereene terrorist attack." *Evidence Technology Magazine*, 10(3):20-23, 2012.

M. W. Perlin. "Forensic science in the information age." *Forensic Magazine*, 9(2):17-21, 2012.

#### *Book chapter (4)*

M. W. Perlin, "The Blairsville slaying and the dawn of DNA computing," in *Death Needs Answers: The Cold-Blooded Murder of Dr. John Yelenic*, A. Niapas, Ed., New Kensington, PA: Grelin Press, 2013.

M. W. Perlin, "DNA Identification Science," in *Forensic Sciences*, volume 3. C. H. Wecht, Ed., Albany, NY: LexisNexis Matthew Bender, Chapter 37C, 2012.

Dr. Mark W. Perlin

M. W. Perlin, "Identifying human remains using TrueAllele® technology." Forensic Investigation and Management of Mass Disasters. M. I. Okoye and C. H. Wecht. Tucson, AZ, Lawyers & Judges Publishing Co: 31-38, 2007.

M. W. Perlin, "Mass casualty identification through DNA analysis: overview, problems and pitfalls." Forensic Investigation and Management of Mass Disasters. M. I. Okoye and C. H. Wecht. Tucson, AZ, Lawyers & Judges Publishing Co: 23-30, 2007.

#### *Newsletter (5)*

M. W. Perlin. "DNA done right." *FHC Experts for Law: Experts Forum Newsletter*, (5):4-7, 2013.

M. W. Perlin. "Cybergenetics TrueAllele technology enables objective analysis of previously unusable DNA evidence." *MathWorks Newsletters: Technical Article*. 1-4, 2013.

M. W. Perlin. "DNA intelligence and forensic failure: what you don't know can kill you." *Cybergenetics: The DNA Investigator™ Newsletter*, Winter, 2011.

M. W. Perlin. "Validating DNA mixture interpretation methods." *Cybergenetics: The DNA Investigator™ Newsletter*, Spring, 2010.

M. W. Perlin. "Same data, more information – murder, match and DNA." *Cybergenetics: The DNA Investigator™ Newsletter*, Fall, 2009.

#### *Thesis (2)*

M. W. Perlin, "Automating the construction of efficient Artificial Intelligence algorithms", Doctoral Dissertation, School of Computer Science, Carnegie Mellon University, 1991.

M. W. Perlin, "Random Graphs Applied to the Immune Network," Doctoral Dissertation, Mathematics Department, City University of New York, 1982.

### **Presentations**

R. David, M. Bowkley\* and M. W. Perlin, "Separating familial mixtures, one genotype at a time", *Northeastern Association of Forensic Scientists 40th Annual Meeting*, Hershey, PA, 2014.

M. W. Perlin, "Solving cold cases by TrueAllele® analysis of DNA evidence", *Finding Closure: The Science, Law and Politics of Cold Case Investigations*, Cyril H. Wecht Institute of Forensic Science and Law 14th Annual Symposium, Pittsburgh, PA, 2014.

J. Hornyak, W. Allan and M. W. Perlin, "Using TrueAllele® Casework to separate DNA mixtures of relatives", *DNA Workshop, 124th California Association of Criminalists*, San Francisco, CA, 2014.

M. Bowkley\* and M. W. Perlin, "Compute first, ask questions later: an efficient TrueAllele® workflow", *Midwestern Association of Forensic Scientists 43rd Annual Fall Meeting*, St. Paul, MN, 2014.



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J. Hornyak\*, W. P. Allan and M. W. Perlin, "TrueAllele® Casework validation on PowerPlex® 21 mixture data", *Twenty Second International Symposium on the Forensic Sciences of the Australia and New Zealand Forensic Science Society (ANZFSS)*, Adelaide, Australia, 2014.

M. W. Perlin, "TrueAllele® interpretation of DNA mixture evidence", Keynote talk, *Ninth International Conference on Forensic Statistics and Inference (ICFIS)*, Leiden, The Netherlands, 2014.

M. W. Perlin, "Solving crimes using MCMC to analyze previously unusable DNA evidence", *American Statistical Association, Joint Statistical Meetings (JSM)*, Boston, MA, 2014.

M. W. Perlin, "Preventing rape in the military through effective DNA computing", *Forensic Europe Expo, Forensic Seminar Theatre*, London, UK, 2014.

M. W. Perlin, "Cracking the DNA mixture code – computer analysis of UK crime cases", *Forensic Europe Expo, Forensic Innovation Conference*, London, UK, 2014.

M. W. Perlin and M. M. Legler, "Coding a safer society through computer interpretation of DNA evidence", *MATLAB Virtual Conference*, Europe and North America, 2014.

M. W. Perlin, "Getting past first Bayes with DNA mixtures", *American Academy of Forensic Sciences 66th Annual Meeting*, Seattle, WA, 2014.

M. W. Perlin, "DNA knowledge, DNA power: how computers interpret evidence", *Cybergenetics Webinar*, Pittsburgh, PA, 2013.

M. W. Perlin, "Unleashing forensic DNA through computer intelligence", *Forensic Europe Expo, Forensic Innovation Conference*, London, UK, 2013.

M. W. Perlin, "Finding truth in DNA mixture evidence", *Innocence Network Conference, Advanced DNA*, Charlotte, NC, 2013.

M. W. Perlin, K. Dormer, J. Hornyak, L. Schiermeier-Wood, and S. Greenspoon, "Virginia TrueAllele® validation study: casework comparison", *American Academy of Forensic Sciences 65th Annual Meeting*, Washington, DC, 2013.

M. W. Perlin, K. Dormer, J. Hornyak, T. Meyers, and W. Lorenz, "How inclusion interpretation of DNA mixture evidence reduces identification information", *American Academy of Forensic Sciences 65th Annual Meeting*, Washington, DC, 2013.

M. W. Perlin, "DNA mapping the crime scene: do computers dream of electric peaks?", *Promega's Twenty Third International Symposium on Human Identification*, Nashville, TN, 2012.

M. W. Perlin, "When good DNA goes bad," *International Conference on Forensic Research and Technology*, Chicago, IL, 2012.

M. W. Perlin, "Forensic thinking, fast and slow," *International Conference on Forensic Research and Technology*, Chicago, IL, 2012.

M. W. Perlin, "The Massereene touch DNA evidence", *Twenty First International Symposium on the Forensic Sciences of the Australian and New Zealand Forensic Science Society*, Hobart, Tasmania, 2012. (Talk presented by DCI John McVea of the Police Service of Northern Ireland.)

Dr. Mark W. Perlin

M. W. Perlin, "Combining DNA evidence for greater match information", *American Academy of Forensic Sciences 64th Annual Meeting*, Atlanta, GA, 2012.

M. W. Perlin, "Investigative DNA databases that preserve identification information", *American Academy of Forensic Sciences 64th Annual Meeting*, Atlanta, GA, 2012.

R. David\* and M. W. Perlin, "Creating informative DNA libraries using computer reinterpretation of existing data", *Northeastern Association of Forensic Scientists 2011 Annual Meeting*, Newport, RI, 2011.

J. Ballantyne and M. W. Perlin, "DNA mixture deconvolution by binomial sampling of individual cells", *Eighth International Conference on Forensic Inference and Statistics*, Seattle, WA, 2011.

M. W. Perlin, "Computer interpretation of uncertain DNA evidence", *National Institute of Justice (NIJ) Conference*, Arlington, VA, 2011.

M. W. Perlin, "Taming uncertainty in forensic DNA evidence", *European Network of Forensic Science Institutes (ENFSI) DNA Working Group meeting*, Brussels, Belgium, 2011.

M. W. Perlin, "Sherlock Holmes and the DNA likelihood ratio", *American Academy of Forensic Sciences 63rd Annual Meeting*, Chicago, IL, 2011.

M. W. Perlin, "The science of quantitative DNA mixture interpretation", *Scientific Working Group on DNA Analysis Methods (SWGDM)*, Fredericksburg, VA, 2011.

M. W. Perlin, "Reliable interpretation of stochastic DNA evidence", *Canadian Society of Forensic Sciences 57th Annual Meeting*, Toronto, ON, 2010.

M. W. Perlin, "Overcoming DNA stochastic effects", *Northeastern Association of Forensic Scientists 2010 Annual Meeting*, Manchester, VT, 2010.

M. W. Perlin, "Inclusion probability is a likelihood ratio: implications for DNA mixtures" (poster), *Promega's Twenty First International Symposium on Human Identification*, San Antonio, TX, 2010.

M. W. Perlin, "Explaining the likelihood ratio in DNA mixture interpretation", *Promega's Twenty First International Symposium on Human Identification*, San Antonio, TX, 2010.

R. David\* and M. W. Perlin, "More informative DNA identification: Computer reinterpretation of existing data", *Midwestern Association of Forensic Scientists*, Kansas City, MO, 2010.

M. W. Perlin and K. E. Williams, "Preserving DNA information", *National Association of Medical Examiners 2010 Annual Meeting*, Cleveland, OH, 2010.

M. W. Perlin and B. W. Duceman, "Profiles in productivity: Greater yield at lower cost with computer DNA interpretation", *Twentieth International Symposium on the Forensic Sciences of the Australian and New Zealand Forensic Science Society*, Sydney, Australia, 2010.

M. W. Perlin and M. Greenhalgh, "Scientific combination of DNA evidence: A handgun mixture in eight parts", *Twentieth International Symposium on the Forensic Sciences of the Australian and New Zealand Forensic Science Society*, Sydney, Australia, 2010.



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M. W. Perlin, "DNA identification science: The search for truth", *Duquesne University 2010 Summer Research Symposium Keynote Address*, Pittsburgh, PA, 2010.

M. W. Perlin, "Statistical computation for forensic DNA evidence", *University of Pittsburgh Department of Human Genetics*, Pittsburgh, PA, 2010.

M. W. Perlin and R. W. Cotton, "Three match statistics, one verdict," *American Academy of Forensic Sciences 62nd Annual Meeting*, Seattle, WA, 2010.

M. W. Perlin and B. W. Duceman, "Casework validation of genetic calculator mixture interpretation," *American Academy of Forensic Sciences 62nd Annual Meeting*, Seattle, WA, 2010.

M. W. Perlin, J. B. Kadane and R. W. Cotton, "A match likelihood ratio for DNA comparison," *American Academy of Forensic Sciences 61st Annual Meeting*, Denver, CO, 2009.

M. W. Perlin, A. Sinelnikov, E. Vey, M. Legler and M. Clarke, "Identifying victim remains from uncertain data," *American Academy of Forensic Sciences 61st Annual Meeting*, Denver, CO, 2009.

M. W. Perlin, J. B. Kadane and R. W. Cotton. "Forensic DNA inference," *Seventh International Conference on Forensic Inference and Statistics*, Lausanne, Switzerland, 2008.

M. W. Perlin, "Exploring Forensic Scenarios with TrueAllele<sup>®</sup> Mixture Automation," *American Academy of Forensic Sciences 59th Annual Meeting*, San Antonio, TX, 2007.

M. W. Perlin, "Scientific validation of mixture interpretation methods," *Promega's Seventeenth International Symposium on Human Identification*. Nashville, TN, 2006.

M. W. Perlin, "Real-time DNA investigation," *Promega's Sixteenth International Symposium on Human Identification*. Dallas, TX, 2005.

M. W. Perlin, "Simple reporting of complex DNA evidence: automated computer interpretation," *Promega's Fourteenth International Symposium on Human Identification*. Phoenix, AZ, 2003.

M.W. Perlin, "Expert systems for automated STR analysis," *Scientific Working Group on DNA Analysis Methods (SWGDM)*, Quantico, VA, 2003.

M. W. Perlin M. W., D. Coffman, C.A. Crouse, F. Konotop, and J.D Ban, "Automated STR data analysis: validation studies," *Promega's Twelfth International Symposium on Human Identification*. Biloxi, MS, 2001.

M. W. Perlin, "An expert system for scoring DNA database profiles," *Promega's Eleventh International Symposium on Human Identification*. Biloxi, MS, 2000.

M. W. Perlin, "Computer automation of STR scoring for forensic databases," *First International Conference on Forensic Human Identification in The Millennium*, London, UK, The Forensic Science Service, 1999.

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## Courses

### *Continuing Legal Education*

M. W. Perlin, "Shedding light on inconclusive DNA: TrueAllele® computer analysis", *Office of the Onondaga County District Attorney*, Syracuse, NY, November, 2014.

M. W. Perlin, "TrueAllele computing: all the DNA, all the time", *NSW Office of the Director of Public Prosecutions, Continuing Professional Development*, Sydney, Australia, March, 2014.

M. W. Perlin, "TrueAllele® interpretation of Allegheny County DNA mixtures", *Allegheny County Courthouse, Continuing Legal Education*, Pittsburgh, PA, February, 2014.

M. W. Perlin, "No DNA left behind: when 'inconclusive' really means 'informative'", *Office of the Schenectady County District Attorney*, Schenectady, NY, January, 2014.

M. W. Perlin, "Understanding DNA mixtures" & "How to convict an innocent man using DNA mixtures" *DNA in the 21<sup>st</sup> Century, New Jersey Office of the Public Defender*, Trenton, NJ, October, 2013.

J. Butler, A. Mitchell, M. W. Perlin, A. M. Schubert, J. Friedman and J. Spriggs, "DNA mixture interpretations and statistics – to include or exclude", *Prescription for Criminal Justice Forensics, American Bar Association Criminal Justice Section*, New York, NY, June, 2013.

M. W. Perlin, "DNA mixture statistics", *Virginia Spring Institute, Commonwealth's Attorneys' Services Council*, Richmond, VA, March, 2013.

G. Hampikian, V. Weedn, M. W. Perlin, A. Blumstein, J. Rangos, K. Mains, L. Irwin, A. Adepoju and W. Oliver, "Whose DNA is it anyway?", *Duquesne University Forensic Fridays, Continuing Legal Education Program on DNA Access*, Pittsburgh, PA, March, 2013.

M. W. Perlin, "Reanimating Zombie™ DNA", *Penn State Dickinson Law School*, State College, PA, September, 2012.

M. W. Perlin, "DNA evidence: computer interpretation, case investigation and court presentation", *Kern County District Attorney's Office, Continuing Legal Education*, Bakersfield, CA, April, 2012.

M. W. Perlin, J. Galloway and M. Agnew, "Investigation and trial in the Massereene case", *Police, Public Prosecution and Forensic Services of Northern Ireland, Continuing Professional Development*, Belfast, Northern Ireland, March, 2012.

M. W. Perlin and J. Galloway, "Touch DNA and the Massereene Barracks attack investigation", *Allegheny County Courthouse, Continuing Legal Education*, Pittsburgh, PA, February, 2012.

R. Freeman, M. W. Perlin and R. Harmon, "The science of DNA search", *Duquesne University Forensic Fridays, Continuing Legal Education Program on Familial Search*, Pittsburgh, PA, May, 2011.

M. W. Perlin and A. Krastek, "Forensic DNA analysis: A CLE introduction", *Allegheny County Courthouse, Continuing Legal Education*, Pittsburgh, PA, March, 2011.

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M. W. Perlin, A. Krastek and M. Collins, "Forensic DNA analysis: An introduction", *Duquesne University Forensic Fridays, Continuing Legal Education*, Pittsburgh, PA, October, 2010.

*Forensic Science Training*

M. W. Perlin, "How TrueAllele® Works, Part 2: Degraded DNA and allele dropout", *Cybergenetics Webinar*, November, 2014.

M. W. Perlin, "How TrueAllele® Works, Part 1: Genotype modeling and the likelihood ratio", *Cybergenetics Webinar*, October, 2014.

M. W. Perlin, "TrueAllele® Casework", *Almost Everything You Wanted to Know About Probabilistic Software (But Were Afraid to Ask)*, *Promega's Twenty Fifth International Symposium on Human Identification*, Phoenix, AZ, September, 2014.

M. W. Perlin, "Computer interpretation of touch DNA mixtures", *Seminar for Chiefs of Police in Western Pennsylvania, CSI Investigators Series*, Pittsburgh, PA, May, 2014.

M. W. Perlin, "Revolutionising DNA analysis in major crime investigations", *The Investigator, Full Day DNA Workshop*, Aylesbury, Buckinghamshire, UK, May, 2014.

M. W. Perlin, "DNA-led investigation through computer interpretation of evidence", *Workshop for Criminal Investigation Assessment*, Pennsylvania State Police Academy, Hershey, PA, April, 2014.

M. W. Perlin, M. Legler, J. Hornyak and L. Ferrara, "Science & Software: DNA mixture interpretation", *Cybergenetics Forensic Science Student Workshop*, George Washington University, Washington, DC (distance learning), October, 2013.

M. W. Perlin, "Revolutionising DNA Analysis in Major Crime Investigations", *Workshop for Investigators*, The Investigator Conferences, Rothley, Leicestershire, UK, April, 2013.

Part 1. The DNA information pathway

Part 2. TrueAllele® case studies

Part 3. The way forward in the UK

M. W. Perlin, "TrueAllele® Mixture Interpretation", *9<sup>th</sup> Annual DNA Technology Educational Seminar*, Centre of Forensic Sciences and the Promega Corporation, Toronto, ON, November, 2012.

M. W. Perlin, "TrueAllele® Challenges in Court and Culture", *9<sup>th</sup> Annual DNA Technology Educational Seminar*, Centre of Forensic Sciences and the Promega Corporation, Toronto, ON, November, 2012.

M. W. Perlin, M. Legler and J. Hornyak, "Science & Software: DNA mixture interpretation" (with hands-on TrueAllele® computer laboratory), *Cybergenetics Forensic Scientist Training Course*, New York State Police (NYSP), Albany, NY (distance learning), October, 2012.

M. W. Perlin, M. Legler, J. Hornyak and K. Dormer, "Science & Software: DNA mixture interpretation" (with hands-on TrueAllele® computer laboratory), *Cybergenetics Forensic Scientist Training Course*, Duquesne University, Pittsburgh, PA, Fall, 2012.

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